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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/939,293	08/24/2001	Emad S. Alnemri	480140.465	2539

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EXAMINER	
DAVIS, MINH TAM B	

ART UNIT	PAPER NUMBER
1642	12

DATE MAILED: 02/27/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/939,293	ALNEMRI, EMAD S.	
	Examiner	Art Unit	
	MINH-TAM DAVIS	1642	

-- The MAILING DATE of this communication appears n the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *19 December 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *28-51* is/are pending in the application.

4a) Of the above claim(s) *32-35,40-43 and 48-51* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *28-31,36-39 and 44-47* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *7,9* .
4) ☒ Interview Summary (PTO-413) Paper No(s). *12*.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Applicant's election without traverse of group II, claims 28-51, 88, in Paper No. 11 is acknowledged.

In a telephonic conversation with William Christiansen, on 02/10/03, Applicant elects species a peptide or a polypeptide of Smac having at least two contiguous amino acid residues derived from at least residues 56-139 of SEQ ID NO:1, and species a combination of BIR1 and BIR2 domains.

It is noted that claims 1-27 and 52-96 have been cancelled, according to the amendment of paper No:6.

Accordingly, group II, claims 28-31, 36-39, 44-47, species a peptide or a polypeptide of Smac having at least two contiguous amino acid residues derived from at least residues 56-139 of SEQ ID NO:1, and species a combination of BIR1 and BIR2 domains are examined in the instant application. Claims 32-35, 40-43, 48-51 are withdrawn from consideration as being drawn to non-elected species.

SEQUENCE RULE COMPLIANCE

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. 1.821-25 for the following reasons:

Figure legends of figures 1 and 7 recite sequences that are not accompanied with sequence identification numbers.

OBJECTION

1. Claims 36-39 are objected to because claims 36-39 are essentially identical to claims 28-31.

Claims 36-39 are objected to because they are drawn to the same composition as claims 28-31, respectively. Claims 36-39 are drawn to a Smac peptide or polypeptide "consisting essentially" of an amino acid sequence having at least two contiguous amino acid residues derived from at least residues 56-139 of SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2. The language "consists essentially" of claims 36-39 is interpreted to mean the same as "comprises" of claims 28-31.

Applicant is advised that should claims 28-31 be found allowable, claims 36-39 will be rejected under 35 U.S.C. 101 as being a substantial duplicate thereof, When two claims in an application are duplicates or else are so close in content that they both cover the same thing, despite a slight difference in wording, it is proper after allowing one claim to reject the other as being a substantial duplicate of the allowed claim. See MPEP 706.03(k).

2. Claims 28-31, 36-39, 44-47 are objected to because SEQ ID NO:1 recited in claims 28, 36 and 44 seems to be a polynucleotide sequence, as disclosed in the sequence listing. Does Applicant mean amino acid residues 56-139 of a polypeptide encoded by SEQ ID NO:1?

3. Claims 28-31, 36-39, 44-47 are objected to it is not clear in claims 28, 36 and 44, a functional variant of each of what and a functional equivalent of each of what.

4. Claims 28-31, 36-39, 44-47 are objected to the use of the language "derived" in claims 28, 36 and 44. It is not clear how the two contiguous amino acid residues are derived from at least residues 56-139 of SEQ ID NO:1.

5. The oath or declaration is defective because:

The residence is not provided in the oath or declaration. See 37 CFR 1.52(c).

This application will not be passed to issue until a new declaration is submitted with (a) a statement acknowledging the duty to disclose material which occurred between the filing date of the prior application and the continuation-in part application, and (b) continuing data that matches the priority claimed in paragraph 1 of page 1 of the specification. See M.P.E.P. § 605.04.filed as provided by 37 C.F.R. § 1.312. To ensure consideration of such an amendment, it **MUST** be submitted no later than the payment of the Issue Fee.

REJECTION UNDER 35 USC 112, FIRST PARAGRAPH, WRITTEN DESCRIPTION

Claims 28-31, 36-39, 44-47 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 28-31, 36-39, 44-47 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence "having" at least two contiguous amino acid

residues derived from at least residues 56-139 of SEQ ID NO:1, "a functional variant" or "a functional equivalent" thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

Due to the objected language of claims 28, 36 and 44, and for the purpose of compact prosecution, it is assumed that claims 28-33, 36-41, 44-49 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence "having" at least two contiguous amino acid residues derived from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

The specification discloses that functional variants may result from natural polymorphisms or may be synthesized by recombinant methodology, and differ from wild-type peptides by one or more amino acid substitutions, insertions, deletions or the like (p.18, second paragraph). The specification further discloses the claimed variants retain at least one biological or functional activity associated with N-terminal domain of Smac, preferably specific binding to at least a portion of an inhibitor of apoptosis protein (IAP) (p.18, second paragraph). The specification further discloses that a functional equivalent of a Smac peptide or polypeptide is a peptide or polypeptide with at least one amino acid substitution and retains at least one functional activity associated with N-terminal domain of Smac, preferably specific binding to at least a portion of an inhibitor of apoptosis protein (IAP) (page 12. second paragraph).

The claims 28-31, 36-39, 44-47 encompass a polypeptide of any length and any structure, provided it comprises two contiguous amino acids from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, and variants thereof, wherein said variants are capable of specifically bind to the BIR domains BIR1 and BIR 2.

It is noted that specifically binding to the BIR domains BIR1 and BIR 2 is a physical property and not a specific function. It is further noted that binding to BIR1/BIR2 domains does not necessarily confer caspase -3 and -7 promoting activity, e.g. the mutant delta 21, which is mature Smac lacking the first 21 amino acid residues, could bind to BIR1/BIR2 domains of XIAP (p.4, lines 8-10), but has undetectable Smac activity (p.43, lines 4-5).

Vas-Cath Inc. V. Mahurkar, 19 USPQ2d 1111, clearly states that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention.* The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117). The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (*See Vas-Cath* at page 1116).

Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 USC 112 is severable from its enablement provision (see page 115).

Although drawn to nucleic acids, the teaching of *The Regents of the University of California v. Eli Lilly* (43 USPQ2d 1398-1412) are clearly relevant to the instant rejection. The court held that a generic statement which defines a genus of nucleic acids by only their functional activity does not provide an adequate written description of

the genus. The court indicated that while Applicants are not required to disclose every species encompassed by a genus, the description of a genus is achieved by the recitation of a representative number of DNA molecules, usually defined by a nucleotide sequence, falling within the scope of the claimed genus. At section B(1), the court states that "An adequate written description of a DNA...'requires a precise definition, such as by structure, formula, chemical name, or physical properties', not a mere wish or plan for obtaining the claimed chemical invention".

The claims 28-31, 36-39, 44-47 however read on variants of a polypeptide encoded by SE ID NO:1, wherein said variants have any type of substitution besides conservative substitution, at any amino acid, throughout the length of the peptide, as well as insertions and deletions. The specification and the claims do not place any limit on which amino acid to be subjected to conservative or non-conservative substitution, the type of substitution besides conservative substitution, nor the type of amino acids replacing the original amino acids. In addition, the specification and all other pending claims do not place any limit on the number of amino acids that could be substituted. Thus the scope of the claims includes structural variants. Although the specification discloses that the types of changes are routinely done in the art, the specification and the claims do not provide any guidance as to which, or how many original amino acid(s) to be substituted, or to which type of substitution besides conservative substitution, or which amino acids could be deleted or inserted so that the claimed polypeptide could function as contemplated. No common structural attributes that identify the claimed variants are disclosed. In addition, no common functional attributes that identify the

claimed variants are disclosed, because the function of a polypeptide sequence could be abolished, even with substitution of only one amino acid (Burgess et al. Journal of Cell Biology, 1990, 11: 2129-2138). In addition, although conservative substitution would not destroy the biological function of a protein, the specification fails to disclose which amino acid(s) would be subjected to conservative substitution. The general knowledge and level of skill in the art do not supplement the omitted description, because specific, not general, guidance is what is needed. Since the disclosure fails to describe the common attributes or characteristics that identify members of the claimed variants, the polypeptide encoded by SEQ ID NO:1 alone is insufficient to describe said variants. One of skill in the art would reasonably conclude that the disclosure fails to provide a representative number of variants. Thus, applicant was not in possession of the claimed variants.

Thus, there is insufficient support of claims 28-31, 36-39, 44-47 as provided by the Interim Written Description Guidelines published in the June 5, 1998 Federal Register at Volume 63, Number 114, pages 32639-32645. Therefore, only a peptide or a polypeptide consisting of an amino acid sequence "consisting of" at least two contiguous amino acid residues derived from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, but not the full breadth of the claim meets the written description provision of 35 USC 112, first paragraph.

Claim Rejections - 35 USC § 112, FIRST PARAGRAPH, SCOPE

1. If Applicant could overcome the above 112, first paragraph rejection, claims 28-31, 36-39, 44-47 are still rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling a peptide or polypeptide consisting at least the first 7 amino acids from residues 56-139 of the polypeptide Smac-L encoded by SEQ ID NO:1, which is capable of specifically bind to the BIR domains BIR1 and BIR2 of the Inhibitor of Apoptosis protein named XIAP, does not reasonably provide enablement for peptide or a polypeptide comprising or consisting of an amino acid sequence having at least any "two contiguous amino acid residues" derived from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

Claims 28-31, 36-39, 44-47 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence "having" at least two contiguous amino acid residues derived from at least residues 56-139 of SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

Due to the objected language of claims 28, 36 and 44, and for the purpose of compact prosecution, it is assumed that claims 28-33, 36-41, 44-49 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence having at least two contiguous amino acid residues derived from at least residues 56-139 of a

polypeptide encoded by SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

Claims 28-33, 36-41, 44-49 encompass a peptide or a polypeptide having as little as "any two contiguous amino acid residues" derived from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

The specification discloses that the peptide Smac-N7 (SEQ ID NO:6), consisting of the first 7 residues of mature Smac (which is the same as the first 7 amino acids from residues 56-139 of the polypeptide Smac-L encoded by SEQ ID NO:1) and the peptide Smac N-35 (SEQ ID NO:11), consisting of the first 35 amino acids of mature Smac, are very effective in promoting caspase-3 activation (p.45, first paragraph). The specification also discloses that an internal Smac sequence, Smac 15-35 (SEQ ID NO:10) is almost inactive. In addition, the specification discloses that a mature Smac mutant, which has the first 4 amino acids deleted (delta 4), or the first 21 amino acid deleted (delta 21), are not able to interact with the BIR3 domain of XIAP, which is important for inhibition of caspase-9 activity, but are still able to interact with the BIR1/BIR2 domains of XIAP, which are important for caspase-3 and -7 inhibition (p. 43, first paragraph, and p. 44, second paragraph). The specification discloses that one N-terminal deletion mutant lacking the first 139 residues (delta 139) is completely inactive (p.43, first paragraph).

It is noted that SEQ ID NO:1 is the same as long Smac isoform (Smac-L) (figure 1), which is identical to the mature Smac, except that the mature Smac does not have the amino acids 1-55 (MTS domain) of Smac-L (SEQ ID NO:1) (p.12, lines 4-10). Thus the first amino acid of mature Smac is the same as amino acid 56 of SEQ ID NO:1.

One cannot extrapolate the teaching in the specification to the claimed invention, because it is unpredictable that a peptide consisting of any two amino acids from the amino acids 56-139 of SEQ ID NO:1, including any two amino acids from the first 7 residues of mature Smac (Smac-N7, or SEQ ID NO:6), and any two amino acids of the first 35 amino acids of mature Smac (Smac N-35, or SEQ ID NO:11), would specifically bind to the BIR1/BIR2 domains of XIAP. It is well known in the art that a specific binding of a ligand to a substrate requires specific interaction between the ligand and the substrate, and correct conformation of the ligand to fit into the binding site of the substrate, e.g. specific binding between a ligand and a receptor, or between an antigen and an antibody. Thus one cannot predict that at least any two amino acids from the amino acids 56-139 of SEQ ID NO:1 would have the necessary conformation for specifically binding to the BIR1/BIR2 domains of XIAP.

In view of the above, it would be undue experimentation for one of skill in the art to practice the claimed invention.

2. If Applicant could overcome the above 112, first paragraph rejection, claims 28-31, 36-39, 44-47 are still rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling a peptide or polypeptide consisting of at least the first 7 amino acids from residues 56-139 of the polypeptide Smac-L encoded by SEQ ID

NO:1, which is capable of specifically bind to the BIR domains BIR1 and BIR2 of the Inhibitor of Apoptosis protein named XIAP, does not reasonably provide enablement for "a functional variant or a functional equivalent " of a peptide or a polypeptide comprising or consisting of an amino acid sequence having at least any two contiguous amino acid residues derived from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

withdrawn cancel

Claims 28-31, 36-39, 44-47 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence "having" at least two contiguous amino acid residues derived from at least residues 56-139 of SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

Due to the objected language of claims 28, 36 and 44, and for the purpose of compact prosecution, it is assumed that claims 28-33, 36-41, 44-49 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence having at least two contiguous amino acid residues derived from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

Claims 28-33, 36-41, 44-49 encompass "a functional variant or a functional equivalent " of a peptide or a polypeptide comprising or consisting of an amino acid sequence having at least any two contiguous amino acid residues derived from at least residues 56-139 of a polypeptide encoded by SEQ ID NO:1, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

The scope of the claims includes numerous structural variants. Applicants have not shown how to make and use the claimed peptide or polypeptide variants which are capable of functioning as that which is being disclosed.

Protein chemistry is probably one of the most unpredictable areas of biotechnology. For example, replacement of a single lysine residue at position 118 of acidic fibroblast growth factor by glutamic acid led to the substantial loss of heparin binding, receptor binding and biological activity of the protein (Burgess et al. Journal of Cell Biology, 1990, 11: 2129-2138). In transforming growth factor alpha, replacement of aspartic acid at position 47 with alanine or asparagine did not affect biological activity while replacement with serine or glutamic acid sharply reduced the biological activity of the mitogen (Lazar et al. Molecular and Cell Biology, 1988, 8: 1247-1252). Similarly, it has been shown that aglycosylation of antibodies reduces the resistance of the antibodies to proteolytic degradation, while CH2 deletions increase the binding affinity of the antibodies (see Tao. et al. The Journal of Immunology, 1989, 143(8): 2595-2601, and Gillies et al. Human Antibodies and Hybridomas, 1990, 1(1): 47-54). These references demonstrate that even a single amino acid substitution or what appears to

be an inconsequential chemical modification will often dramatically affect the biological activity and characteristic of a protein.

In view of the above unpredictability, one of skill in the art would be forced into undue experimentation in order to perform the claimed invention as broadly as claimed.

In addition, although conservative subsititution would not destroy the biological function of a protein, the specification fails to disclose which amino acid(s) would be subjected to conservative substitution. In the absence of a source of method of making such variants, one of skill in the art would be forced into undue experimentation to practice the claimed invention as broadly as claimed.

REJECTION UNDER 35 USC 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) do not apply to the examination of this application as the application being examined was not (1) filed on or after November 29, 2000, or (2) voluntarily published under 35 U.S.C. 122(b). Therefore, this application is examined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

1. Claims 28, 36, 44 are rejected under 35 U.S.C. 102(e) as being anticipated by Heilig R et al, Genbank Sequence Database (Accession S02013), National Center for Biotechnology Information, National Library of Medicine, Bethesda, Maryland, publicly available on 1987

Claims 28, 36, 44 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence "having" at least two contiguous amino acid residues derived from at least residues 56-139 of SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

Due to the objected language of claims 28, 36 and 44, and for the purpose of compact prosecution, it is assumed that claims 28, 36, 44 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence having at least two contiguous amino acid residues derived from at least residues 56-139 of the polypeptide encoded by SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

It is noted that residues 56-57 of the polypeptide encoded by SEQ ID NO:1 are amino acids Ala-Val, encoded by nucleotides 185-190 of SEQ ID NO:1 (see sequence listing).

Heilig R et al teach an amino acid sequence comprising the amino acids Ala-Val, as shown by sequence similarity search (MPSRCH search report, 2003, us-09-939-293-1.rpr, pages 3-4). Heilig R et al do not teach that the polypeptide is capable of specifically bind to the BIR domains BIR1 and BIR 2.

The reference does not specifically teach that the polypeptide is capable of specifically bind to the BIR domains BIR1 and BIR 2. However, the claimed peptides or polypeptides appears to be the same as the prior art polypeptide. The office does not have the facilities and resources to provide the factual evidence needed in order to establish that the product of the prior art does not possess the same material, structural and functional characteristics of the claimed product. In the absence of evidence to the contrary, the burden is on the applicant to prove that the claimed product is different from those taught by the prior art and to establish patentable differences. See In re Best 562F.2d 1252, 195 USPQ 430 (CCPA 1977) and Ex parte Gray 10 USPQ 2d 1922 (PTO Bd. Pat. App. & Int. 1989).

2. Claims 28, 36, 44 are rejected under 35 U.S.C. 102(e) as being anticipated by.US 6,110691

Claims 28, 36, 44 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence "having" at least two contiguous amino acid residues derived from at least residues 56-139 of SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

Due to the objected language of claims 28, 36 and 44, and for the purpose of compact prosecution, it is assumed that claims 28, 36, 44 are drawn to a peptide or a polypeptide comprising or consisting of an amino acid sequence having at least two contiguous amino acid residues derived from at least residues 56-139 of the polypeptide

encoded by SEQ ID NO:1, a functional variant or a functional equivalent thereof, each of which is capable of specifically bind to the BIR domains BIR1 and BIR 2.

US 6,110691 teaches a Smac polypeptide encoded by SEQ ID NO:1 (column 21-22), which is exactly the same as the Smac polypeptide encoded by SEQ ID NO:1 in the claimed invention (see sequence listing), from amino acid 1 to a 239, as shown in MPSRCH sequence similarity search (MPSRCH search report, 2003, us-09-939-293-1.rag, pages 1-2). US 6,110691 further teaches that the Smac polypeptide activates Caspase-3 (columns 12-16). US 6,110691 does not teach that the Smac polypeptide is capable of specifically bind to the BIR domains BIR1 and BIR 2.

The reference does not specifically teach that the polypeptide is capable of specifically bind to the BIR domains BIR1 and BIR 2. However, the claimed peptides or polypeptides appears to be the same as the prior art polypeptide. The office does not have the facilities and resources to provide the factual evidence needed in order to establish that the product of the prior art does not possess the same material, structural and functional characteristics of the claimed product. In the absence of evidence to the contrary, the burden is on the applicant to prove that the claimed product is different from those taught by the prior art. See In re Best 562F.2d 1252, 195 USPQ 430 (CCPA 1977) and Ex parte Gray 10 USPQ 2d 1922 (PTO Bd. Pat. App. & Int. 1989).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to MINH-TAM DAVIS whose telephone number is 703-305-2008. The examiner can normally be reached on 9:30AM-4:00PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, ANTHONY CAPUTA can be reached on 703-308-3995. The fax phone numbers for the organization where this application or proceeding is assigned are 703-872-9306 for regular communications and 703-872-9307 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0916.

MINH TAM DAVIS

February 17, 2003

ANTHONY C. CAPUTA
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600